

1/18

SEQUENCE LISTING

<110> The Scripps Research Institute et al.

<120> METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
ANGIOGENESIS USING TYROSINE KINASE SRC

<130> TSRI 651.1

<140> Not yet known

<141> To be determined

<150> 60/087,220

<151> 1998-05-29

<160> 6

<170> PatentIn Ver. 2.0

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<211> 11627

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:RCASBP(A) based
on avian sarcoma virus

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<223> pBR322 sequences

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<222> (5074)..(5077)
<223> env splice acceptor (AGGC)

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 <222> (6879)..(6881)
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																Met Gly	
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agc	agc	aag	agc	aag	ccc	aag	gac	ccc	agc	cag	cgc	cgg	cgc	agc	ctg	165	
Ser	Ser	Lys	Ser	Lys	Pro	Lys	Asp	Pro	Ser	Gln	Arg	Arg	Arg	Ser	Leu		
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gag	cca	ccc	gac	agc	acc	cac	cac	ggg	gga	ttc	cca	gcc	tcg	cag	acc	213	
Glu	Pro	Pro	Asp	Ser	Thr	His	His	Gly	Gly	Phe	Pro	Ala	Ser	Gln	Thr		
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ccc	aac	aag	aca	gca	gcc	ccc	gac	acg	cac	cgc	acc	ccc	agc	cgc	tcc	261	
Pro	Asn	Lys	Thr	Ala	Ala	Pro	Asp	Thr	His	Arg	Thr	Pro	Ser	Arg	Ser		
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ttt	ggg	acc	gtg	gcc	acc	gag	ccc	aag	ctc	ttc	ggg	ggc	ttc	aac	act	309	
Phe	Gly	Thr	Val	Ala	Thr	Glu	Pro	Lys	Leu	Phe	Gly	Gly	Phe	Asn	Thr		
			55							60					65		
tct	gac	acc	gtt	acg	tcg	ccg	cag	cgt	gcc	ggg	gca	ctg	gct	ggc	ggc	357	
Ser	Asp	Thr	Val	Thr	Ser	Pro	Gln	Arg	Ala	Gly	Ala	Leu	Ala	Gly	Gly		
			70							75					80		
gtc	acc	act	ttc	gtg	gct	ctc	tac	gac	tac	gag	tcc	cgg	act	gaa	acg	405	
Val	Thr	Thr	Phe	Val	Ala	Leu	Tyr	Asp	Tyr	Glu	Ser	Arg	Thr	Glu	Thr		
		85					90					95					
gac	ttg	tcc	ttc	aag	aaa	gga	gaa	cgc	ctg	cag	att	gtc	aac	aac	acg	453	
Asp	Leu	Ser	Phe	Lys	Lys	Gly	Glu	Arg	Leu	Gln	Ile	Val	Asn	Asn	Thr		
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gaa	ggg	gac	tgg	tgg	ctg	gct	cat	tcc	ctc	act	aca	gga	cag	acg	ggc	501	
Glu	Gly	Asp	Trp	Trp	Leu	Ala	His	Ser	Leu	Thr	Thr	Gly	Gln	Thr	Gly		
		115					120					125				130	
tac	atc	ccc	agt	aac	tat	gtc	gcg	ccc	tca	gac	tcc	atc	cag	gct	gaa	549	
Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Ser	Asp	Ser	Ile	Gln	Ala	Glu		
			135							140					145		
gag	tgg	tac	ttt	ggg	aag	atc	act	cgt	cgg	gag	tcc	gag	cgg	ctg	ctg	597	
Glu	Trp	Tyr	Phe	Gly	Lys	Ile	Thr	Arg	Arg	Glu	Ser	Glu	Arg	Leu	Leu		
		150							155					160			
ctc	aac	ccc	gaa	aac	ccc	cgg	gga	acc	ttc	ttg	gtc	cgg	gag	agc	gag	645	
Leu	Asn	Pro	Glu	Asn	Pro	Arg	Gly	Thr	Phe	Leu	Val	Arg	Glu	Ser	Glu		
		165					170					175					
acg	aca	aaa	ggg	gcc	tat	tgc	ctc	tcc	gtt	tct	gac	ttt	gac	aac	gcc	693	
Thr	Thr	Lys	Gly	Ala	Tyr	Cys	Leu	Ser	Val	Ser	Asp	Phe	Asp	Asn	Ala		
		180					185					190					
aag	ggg	ctc	aat	gtg	aag	cac	tac	aag	atc	cgc	aag	ctg	gac	agc	ggc	741	
Lys	Gly	Leu	Asn	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Ser	Gly		
		195					200					205				210	
ggc	ttc	tac	atc	acc	tca	cgc	aca	cag	ttc	agc	agc	ctg	cag	cag	ctg	789	
Gly	Phe	Tyr	Ile	Thr	Ser	Arg	Thr	Gln	Phe	Ser	Ser	Leu	Gln	Gln	Leu		
			215							220					225		
gtg	gcc	tac	tac	tcc	aaa	cat	gct	gat	ggc	ttg	tgc	cac	cgc	ctg	acc	837	
Val	Ala	Tyr	Tyr	Ser	Lys	His	Ala	Asp	Gly	Leu	Cys	His	Arg	Leu	Thr		
			230							235					240		
aac	gtc	tgc	ccc	acg	tcc	aag	ccc	cag	acc	cag	gga	ctc	gcc	aag	gac	885	

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Asn	Val	Cys	Pro	Thr	Ser	Lys	Pro	Gln	Thr	Gln	Gly	Leu	Ala	Lys	Asp	
245							250					255				
gcg	tgg	gaa	atc	ccc	cgg	gag	tcg	ctg	cgg	ctg	gag	gtg	aag	ctg	ggg	933
Ala	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Arg	Leu	Glu	Val	Lys	Leu	Gly	
260						265					270					
cag	ggc	tgc	ttt	gga	gag	gtc	tgg	atg	ggg	acc	tgg	aac	ggc	acc	acc	981
Gln	Gly	Cys	Phe	Gly	Glu	Val	Trp	Met	Gly	Thr	Trp	Asn	Gly	Thr	Thr	
275					280					285					290	
aga	gtg	gcc	ata	aag	act	ctg	aag	ccc	ggc	acc	atg	tcc	ccg	gag	gcc	1029
Arg	Val	Ala	Ile	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Pro	Glu	Ala	
				295					300					305		
ttc	ctg	cag	gaa	gcc	caa	gtg	atg	aag	aag	ctc	cgg	cat	gag	aag	ctg	1077
Phe	Leu	Gln	Glu	Ala	Gln	Val	Met	Lys	Lys	Leu	Arg	His	Glu	Lys	Leu	
			310					315					320			
gtt	cag	ctg	tac	gca	gtg	gtg	tcg	gaa	gag	ccc	atc	tac	atc	gtc	act	1125
Val	Gln	Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	
			325				330					335				
gag	tac	atg	agc	aag	ggg	agc	ctc	ctg	gat	ttc	ctg	aag	gga	gag	atg	1173
Glu	Tyr	Met	Ser	Lys	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Gly	Glu	Met	
						345					350					
ggc	aag	tac	ctg	cgg	ctg	cca	cag	ctc	gtc	gat	atg	gct	gct	cag	att	1221
Gly	Lys	Tyr	Leu	Arg	Leu	Pro	Gln	Leu	Val	Asp	Met	Ala	Ala	Gln	Ile	
355					360					365					370	
gca	tcc	ggc	atg	gcc	tat	gtg	gag	agg	atg	aac	tac	gtg	cac	cga	gac	1269
Ala	Ser	Gly	Met	Ala	Tyr	Val	Glu	Arg	Met	Asn	Tyr	Val	His	Arg	Asp	
				375					380					385		
ctg	cgg	gcg	gcc	aac	atc	ctg	gtg	ggg	gag	aac	ctg	gtg	tgc	aag	gtg	1317
Leu	Arg	Ala	Ala	Asn	Ile	Leu	Val	Gly	Glu	Asn	Leu	Val	Cys	Lys	Val	
			390					395					400			
gct	gac	ttt	ggg	ctg	gca	cgc	ctc	atc	gag	gac	aac	gag	tac	aca	gca	1365
Ala	Asp	Phe	Gly	Leu	Ala	Arg	Leu	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	
			405				410					415				
cgg	caa	ggt	gcc	aag	ttc	ccc	atc	aag	tgg	aca	gcc	ccc	gag	gca	gcc	1413
Arg	Gln	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	
			420			425					430					
ctc	tat	ggc	cgg	ttc	acc	atc	aag	tcg	gat	gtc	tgg	tcc	ttc	ggc	atc	1461
Leu	Tyr	Gly	Arg	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	
435					440					445					450	
ctg	ctg	act	gag	ctg	acc	acc	aag	ggc	cgg	gtg	cca	tac	cca	ggg	atg	1509
Leu	Leu	Thr	Glu	Leu	Thr	Thr	Lys	Gly	Arg	Val	Pro	Tyr	Pro	Gly	Met	
				455					460					465		
gtc	aac	agg	gag	gtg	ctg	gac	cag	gtg	gag	agg	ggc	tac	cgc	atg	ccc	1557
Val	Asn	Arg	Glu	Val	Leu	Asp	Gln	Val	Glu	Arg	Gly	Tyr	Arg	Met	Pro	
			470					475					480			
tgc	ccg	ccc	gag	tgc	ccc	gag	tcg	ctg	cat	gac	ctc	atg	tgc	cag	tgc	1605
Cys	Pro	Pro	Glu	Cys	Pro	Glu	Ser	Leu	His	Asp	Leu	Met	Cys	Gln	Cys	
			485				490					495				
tgg	cgg	agg	gac	cct	gag	gag	cgg	ccc	act	ttt	gag	tac	ctg	cag	gcc	1653

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Trp Arg Arg Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ala
 500 505 510
 ttc ctg gag gac tac ttc acc tcg aca gag ccc cag tac cag cct gga 1701
 Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro Gln Tyr Gln Pro Gly
 515 520 525 530
 gag aac cta taggcctgga gctcctcctg gaccagagge ctcgctgtgg ggtacaggg 1759
 Glu Asn Leu

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 <212> PRT
 <213> Chicken

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 Ser Leu Glu Pro Pro Asp Ser Thr His His Gly Gly Phe Pro Ala Ser
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 35 40 45
 Arg Ser Phe Gly Thr Val Ala Thr Glu Pro Lys Leu Phe Gly Gly Phe
 50 55 60
 Asn Thr Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Ala Leu Ala
 65 70 75 80
 Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser Arg Thr
 85 90 95
 Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile Val Asn
 100 105 110
 Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Thr Thr Gly Gln
 115 120 125
 Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp Ser Ile Gln
 130 135 140
 Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg
 145 150 155 160
 Leu Leu Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu
 165 170 175
 Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Asp
 180 185 190
 Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu Asp
 195 200 205
 Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu Gln
 210 215 220
 Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His Arg
 225 230 235 240
 Leu Thr Asn Val Cys Pro Thr Ser Lys Pro Gln Thr Gln Gly Leu Ala
 245 250 255

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Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys
 260 265 270
 Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly
 275 280 285
 Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro
 290 295 300
 Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu
 305 310 315 320
 Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile
 325 330 335
 Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly
 340 345 350
 Glu Met Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala
 355 360 365
 Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His
 370 375 380
 Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys
 385 390 395 400
 Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr
 405 410 415
 Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu
 420 425 430
 Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe
 435 440 445
 Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro
 450 455 460
 Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg
 465 470 475 480
 Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys
 485 490 495
 Gln Cys Trp Arg Arg Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu
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 Pro Gly Glu Asn Leu
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 <212> DNA
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<223> human c-SRC cDNA

<220>

<221> CDS

<222> (134)..(1483)

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agctcctgag aag atg tca gca ata cag gcc gcc tgg cca tcc ggt aca 169
      Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr
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gaa tgt att gcc aag tac aac ttc cac ggc act gcc gag cag gac ctg 217
Glu Cys Ile Ala Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu
      15             20             25

ccc ttc tgc aaa gga gac gtg ctc acc att gtg gcc gtc acc aag gac 265
Pro Phe Cys Lys Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp
      30             35             40

ccc aac tgg tac aaa gcc aaa aac aag gtg ggc cgt gag ggc atc atc 313
Pro Asn Trp Tyr Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile
      45             50             55             60

cca gcc aac tac gtc cag aag cgg gag ggc gtg aag gcg ggt acc aaa 361
Pro Ala Asn Tyr Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys
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ctc agc ctc atg cct tgg ttc cac ggc aag atc aca cgg gag cag gct 409
Leu Ser Leu Met Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala
      80             85             90

gag cgg ctt ctg tac ccg ccg gag aca ggc ctg ttc ctg gtg cgg gag 457
Glu Arg Leu Leu Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu
      95             100             105

agc acc aac tac ccc gga gac tac acg ctg tgc gtg agc tgc gac ggc 505
Ser Thr Asn Tyr Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly
      110             115             120

aag gtg gag cac tac cgc atc atg tac cat gcc agc aag ctc agc atc 553
Lys Val Glu His Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile
      125             130             135             140

gac gag gag gtg tac ttt gag aac ctc atg cag ctg gtg gag cac tac 601
Asp Glu Glu Val Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr
      145             150             155

acc tca gac gca gat gga ctc tgt acg cgc ctc att aaa cca aag gtc 649
Thr Ser Asp Ala Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val
      160             165             170

atg gag ggc aca gtg gcg gcc cag gat gag ttc tac cgc agc ggc tgg 697
Met Glu Gly Thr Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp
      175             180             185

gcc ctg aac atg aag gag ctg aag ctg ctg cag acc atc ggg aag ggg 745
Ala Leu Asn Met Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly
      190             195             200

gag ttc gga gac gtg atg ctg ggc gat tac cga ggg aac aaa gtc gcc 793

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Glu Phe Gly Asp Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala	
205 210 215 220	
gtc aag tgc att aag aac gac gcc act gcc cag gcc ttc ctg gct gaa	841
Val Lys Cys Ile Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu	
225 230 235	
gcc tca gtc atg acg caa ctg cgg cat agc aac ctg gtg cag ctc ctg	889
Ala Ser Val Met Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu	
240 245 250	
ggc gtg atc gtg gag gag aag ggc ggg ctc tac atc gtc act gag tac	937
Gly Val Ile Val Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr	
255 260 265	
atg gcc aag ggg agc ctt gtg gac tac ctg cgg tct agg ggt cgg tca	985
Met Ala Lys Gly Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser	
270 275 280	
gtg ctg ggc gga gac tgt ctc ctc aag ttc tcg cta gat gtc tgc gag	1033
Val Leu Gly Gly Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu	
285 290 295 300	
gcc atg gaa tac ctg gag ggc aac aat ttc gtg cat cga gac ctg gct	1081
Ala Met Glu Tyr Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala	
305 310 315	
gcc cgc aat gtg ctg gtg tct gag gac aac gtg gcc aag gtc agc gac	1129
Ala Arg Asn Val Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp	
320 325 330	
ttt ggt ctc acc aag gag gcg tcc agc acc cag gac acg ggc aag ctg	1177
Phe Gly Leu Thr Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu	
335 340 345	
cca gtc aag tgg aca gcc cct gag gcc ctg aga gag aag aaa ttc tcc	1225
Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser	
350 355 360	
act aag tct gac gtg tgg agt ttc gga atc ctt ctc tgg gaa atc tac	1273
Thr Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr	
365 370 375 380	
tcc ttt ggg cga gtg cct tat cca aga att ccc ctg aag gac gtc gtc	1321
Ser Phe Gly Arg Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val	
385 390 395	
cct cgg gtg gag aag ggc tac aag atg gat gcc ccc gac ggc tgc ccg	1369
Pro Arg Val Glu Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro	
400 405 410	
ccc gca gtc tat gaa gtc atg aag aac tgc tgg cac ctg gac gcc gcc	1417
Pro Ala Val Tyr Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala	
415 420 425	
atg cgg ccc tcc ttc cta cag ctc cga gag cag ctt gag cac atc aaa	1465
Met Arg Pro Ser Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys	
430 435 440	
acc cac gag ctg cac ctg tgacggctgg cctccgctg ggtcatgggc	1513
Thr His Glu Leu His Leu	
445 450	
ctgtgggggac tgaacctgga agatcatgga cctgggtgcc ctgctcactg ggcccgagcc	1573

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 aaggaggcca cggagcggga ggcagcgccc caccacgtcg ggcttccctg gcctcccgcc 1753
 actcgcttc ttagagtttt attcctttcc ttttttgaga tttttttcc gtgtgtttat 1813
 tttttattat ttttcaagat aaggagaaag aaagtaccca gcaaattggc attttacaag 1873
 aagtacgaat cttatttttc ctgtcctgcc cgtgaggggtg ggggggaccg ggccctctc 1933
 tagggacccc tcgccccagc ctcattcccc attctgtgtc ccatgtcccg tgtctcctcg 1993
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 aaaaaaaaaa aaaa 2187

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 <213> Homo sapiens

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 Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
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 Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
 35 40 45
 Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
 50 55 60
 Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
 65 70 75 80
 Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
 85 90 95
 Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
 100 105 110
 Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
 115 120 125
 Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
 130 135 140
 Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
 145 150 155 160
 Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
 165 170 175
 Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met

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180										185					190				
Lys	Glu	Leu	Lys	Leu	Leu	Gln	Thr	Ile	Gly	Lys	Gly	Glu	Phe	Gly	Asp				
		195					200					205							
Val	Met	Leu	Gly	Asp	Tyr	Arg	Gly	Asn	Lys	Val	Ala	Val	Lys	Cys	Ile				
	210					215					220								
Lys	Asn	Asp	Ala	Thr	Ala	Gln	Ala	Phe	Leu	Ala	Glu	Ala	Ser	Val	Met				
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Thr	Gln	Leu	Arg	His	Ser	Asn	Leu	Val	Gln	Leu	Leu	Gly	Val	Ile	Val				
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Glu	Glu	Lys	Gly	Gly	Leu	Tyr	Ile	Val	Thr	Glu	Tyr	Met	Ala	Lys	Gly				
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Ser	Leu	Val	Asp	Tyr	Leu	Arg	Ser	Arg	Gly	Arg	Ser	Val	Leu	Gly	Gly				
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Asp	Cys	Leu	Leu	Lys	Phe	Ser	Leu	Asp	Val	Cys	Glu	Ala	Met	Glu	Tyr				
	290					295				300									
Leu	Glu	Gly	Asn	Asn	Phe	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val				
	305				310					315				320					
Leu	Val	Ser	Glu	Asp	Asn	Val	Ala	Lys	Val	Ser	Asp	Phe	Gly	Leu	Thr				
				325					330					335					
Lys	Glu	Ala	Ser	Ser	Thr	Gln	Asp	Thr	Gly	Lys	Leu	Pro	Val	Lys	Trp				
			340					345					350						
Thr	Ala	Pro	Glu	Ala	Leu	Arg	Glu	Lys	Lys	Phe	Ser	Thr	Lys	Ser	Asp				
		355					360					365							
Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu	Trp	Glu	Ile	Tyr	Ser	Phe	Gly	Arg				
	370					375				380									
Val	Pro	Tyr	Pro	Arg	Ile	Pro	Leu	Lys	Asp	Val	Val	Pro	Arg	Val	Glu				
	385				390					395				400					
Lys	Gly	Tyr	Lys	Met	Asp	Ala	Pro	Asp	Gly	Cys	Pro	Pro	Ala	Val	Tyr				
				405					410					415					
Glu	Val	Met	Lys	Asn	Cys	Trp	His	Leu	Asp	Ala	Ala	Met	Arg	Pro	Ser				
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Phe	Leu	Gln	Leu	Arg	Glu	Gln	Leu	Glu	His	Ile	Lys	Thr	His	Glu	Leu				
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His	Leu																		
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WO 99/61590

PCT/US99/11780

18/18

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